FIG. 1

ACETOACETYL CoA

(D)-3-HYDROXYBUTYRYL-CoA

The state and man area were to some at most state and some are sure and the sound state and some are sure and some state and some sure and som

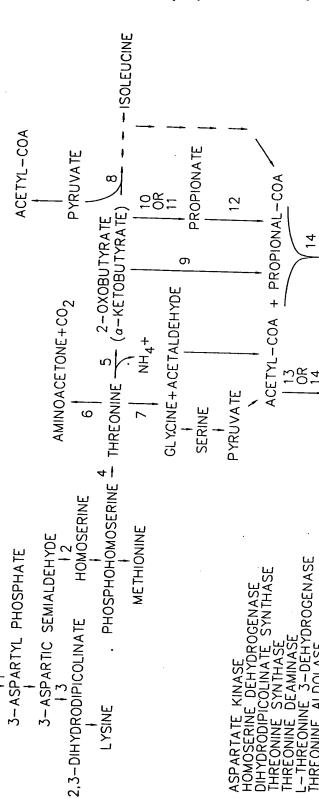
FIG. 2

3-KETOVALERYL COA

Ti M

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ASPARTATE



2. HOMOSERINE DEHYDROGENASE
3. DIHYDRODIPICOLINATE SYNTHASE
5. THREONINE DEAMINASE
6. L-THREONINE J-DEHYDROGENASE
7. THREONINE ALDOLASE
8. ACETOHYDROXYACID SYNTHASE
9. PYRUVATE DEHYDROGENASE COMPLEX
10. PYRUVATE OEHYDROGENASE (E1)
11. a-KETOACID DEHYDROGENASE (E1)
12. ACYL-COA SYNTHETASE
13. PhbA & -KETOTHIOLASE

25.45.667.86

PhbA B-KETOTHIOLASE
BktB B-KETOTHIOLASE
PhbB REDUCTASE
PHA SYNTHASE

R-(-)-3-HYDROXYVALERYL-COA16 R-(-)-3-HYDROXYBUTYRYL-COA

3-KETOVALERYL-COA

ACETOACETYL-COA

P(3HB-co-3HV)COPOLYMER

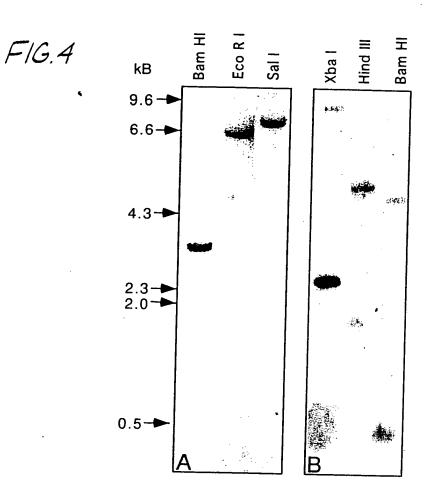


FIG.5

The first control of the first state of the first first state of the f

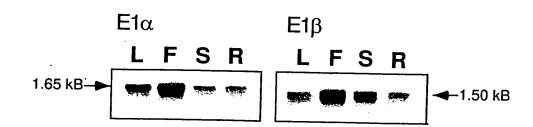
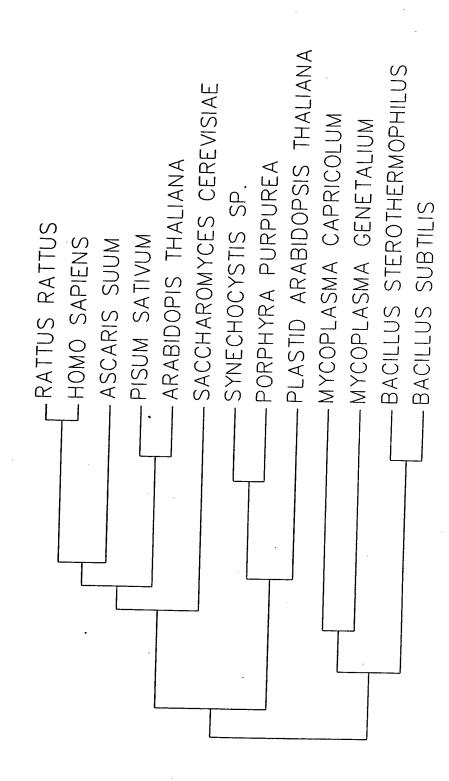


FIG. 6A



THE REAL PROPERTY AND THE PARTY AND THE PART

O.G. FIG. CLASS SUBCLASS

FIG. 6B

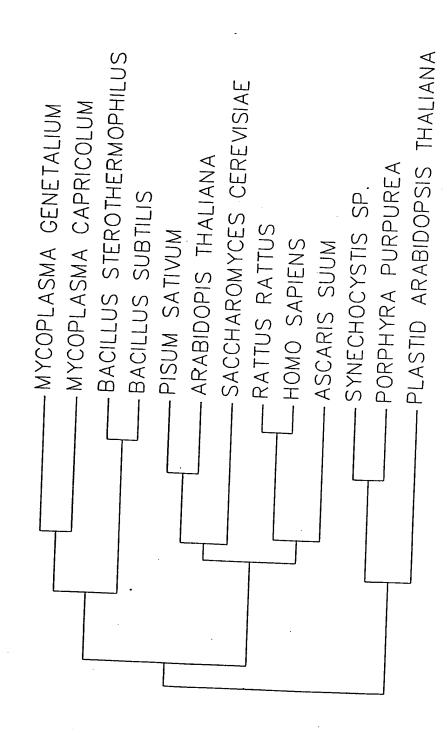
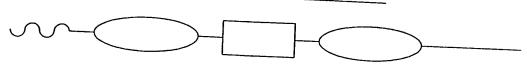
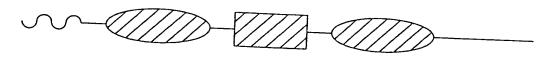


FIG. 7A

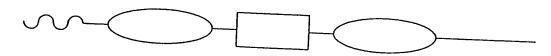
BRANCHED-CHAIN E1a



PLASTID E1a



PLASTID TARGETED BRANCHED-CHAIN E1a CHIMERA



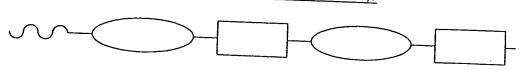
CONSTRUCT 1: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF E1a TO THE BRANCHED-CHAIN E1a. THIS CREATES A PLASTID TARGETED BRANCHED-CHAIN E1a CHIMERA.

And the state and the state of the state of

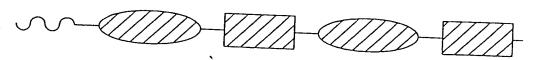
8/19

FIG. 7B

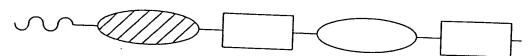
BRANCHED-CHAIN E1B



PLASTID E1B

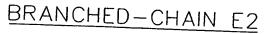


PLASTID TARGETED BRANCHED-CHAIN E18 CHIMERA



CONSTRUCT 2: REPLACE THE N-TERMINUS OF THE BRANCHED-CHAIN E1 β (INCLUDING THE E2 BINDING DOMAIN) WITH THE N-TERMINUS OF THE PLASTID E1 β (INCLUDING THE CHLOROPLAST TARGETING PEPTIDE AND THE PLASTID E2 BINDING DOMAIN). THIS CREATES A PLASTID TARGETED BRANCHED-CHAIN E1 β CHIMERA.

FIG. 7C





PLASTID E2



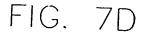
PLASTID TARGETED BRANCHED-CHAIN E2

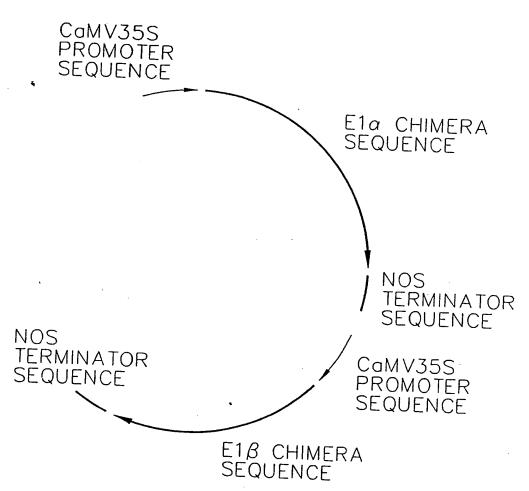


CONSTRUCT 3: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF THE PLASTID E2 TO THE MATURE PORTION OF THE BRANCHED—CHAIN E2, TO CREATE A PLASTID TARGETED BRANCHED—CHAIN E2 CHIMERA.

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10/19



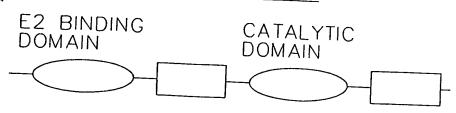


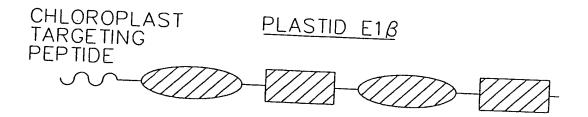
CONSTRUCT 4: MEGA PLASMID CODING FOR BOTH CHIMERIC (PLASTID TARGETED BRANCHED-CHAIN) SUBUNITS IF THE PDH. ATTACH THE E1a CHIMERIC SEQUENCE. TO THE E1B CHIMERIC SEQUENCE WITH TRANSCRIPTION TERMINATOR AND PROMOTER SEQUENCES BETWEEN THE TWO.

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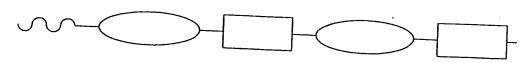
FIG. 7E

BRANCHED-CHAIN E1B





PLASTID TARGETED BRANCHED-CHAIN E18 CHIMERA



CONSTRUCT 5: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF THE PLASTID $E1\beta$ TO THE MATURE PORTION OF THE BRANCHED—CHAIN $E1\beta$. THIS CREATES A PLASTID TARGETED BRANCHED—CHAIN $E1\beta$ CHIMERA.

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FIG. 8A

Plastid A.t.	MATAFAPTKLTATVPLHGSHENRLLLPIRLAPPSSFLGSTRSLSLRRLNH	50
r.purpurea		
A.thaliana	MALSRLSSRSNIITRPFSAAFSRLIS	26
H.sapiens II	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	27
s.cerevisiae	~MLAASFKRQPSQLVRGLGAVLRTPTRIGHVPTMATI KTTDKKARED.	47
A.Suum 1	MIEVEANTEVIORUS COMPTON	23
M.capricolum	AMDST.	4
B.subtilis	MGVKTFQFPFAEQL	14
Consensus		50
SNATERS	PVVSVOEVVKEKOSTANITCI I TEVEROSTANITCI I	
	PVVSVQEVVKEKQSTNNTSLLITKEEGLELYEDMILGRSFEDM	100
TDTTPTT	MSYPKKVELPLTNCNQINLTKHKLLVLYEDMLLGRNFEDM	40
RNFANDA	IETSLPFTAHLCDPPSRSVESSSQELLD-FFRTMALMRRMEIA	75
EGSDTVO	TFEIKKCDLHRLEEGPPVTTVLTREDGLKYYRMMQTVRRMELK	77
RI.ASTEA	IELPESSFESYMLEPPDLSYETSKATLLQMYKDMVIIRRMEMA	97
GKEDDI.KI	TFQTKPFKLHKLDSGPDINVHVTKEDAVHYYTQMLTIRRMESA	73
FKVAFOE	NEKVCVLDKDGKVINPKLMPKISDQEILEAYKIMNLSRRQDIY	54
DICVALQE	PTFQILNEEGEVVNEEAMPELSDEQLKE-LMRRMVYTRILDQR	63
• • • • • • • • • • • • • • • • • • • •	LYMRR.E	100
,	0	
CAQMYYRO	KMFGFVHLYNGQEAVSTGFIKLLTKSDSVVSTYRDHVHALSK	150
CAQMYYKO	KMFGFVHLYNGQEAVSTGVIKLLDSKDYVCSTYRDHVHALSK	150
ADSLYKAN	VIRGFCHLYDGQEAVAIGMEAAITKKDAIITAYRDHCIFLGR	90
ADQLYKQK	IIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRAHGFTFTR	125
CDALYKAK	KIRGFCHLSVGQEAIAVGIENAITKLDSIITSYRCHGFTFMR	127
AGNLYKEK	KVRGFCHLYSGQEACAVGTKAAMDAGDAAVTAYRCHGWTYLS	147
QNTMQRQG	RLLSFLSSTGQEACEVAYINALNKKTDHFVSGYRNNAAWLAM	123
SISLNRQG	RL-GFYAPTAGQEASQIASHFALEKEDFILPGYRDVPQIIWH	104
_	T X	112
LY	GF.HLGQEAGK.DYR.H	150

Ann cons. cons. mass cons. com and care cons. co

FIG. 8B

TPP-binding site	
GVSARAVMSELFGKVTGCCRGQGGSMHMFSKEHNMLGGFAFIGEGIPVAT	200
GVPSQNVMAELFGKETGCSRGRGGSMHIFSAPHNFLGGFAFIAEGIDVAT	140
GGSLHEVFSELMGRQAGCSKGKGGSMHFYKKESSFYGGHGTYGAOVDLGG	175
GLSVREILAELIGRKGGCAKGKGGSMHMYAKN FYGGNGIVGA OVDI GA	175
GASVKAVLAELMGRRAGVSYGKGGSMHLYAPGFYCGNGIYCAOVDLCA	195
GSSVAKVLCELTGRITGNVYGKGGSMHMYGEN FYGGNGIVGNOODIGT	
GQLVRNIMLYWIGNEAG-GKAPEG-VNCLPPNIVIGGOVCOAT	171
GLPLYQAFLFSRGHFHG-NQIPEG-VNVLPPQIIIGAQYIQAA	145
	153
G.SVEL.GGG.GGSMHF.GGI.GAQ.P	200
- · · · · · · · · · · · · · · · · · · ·	200
PDH β binding site	
GAAFSKYRREVLKQDCD-DVTVAFFGDGTCNNGQFFECLNMAALYKLPI	
GAAFQSIYRQQVLKEPGELRVTACFFGDGTTNNGQFFECLNMAVLWKLPI	249
GIAFAQKYNKEEAVTFALYGDGAANQGQLFEALNISALWDLPA	190
GIALACKYNGKDEVCLTLYGDGAANQGQIFEAYNMAALWKLPC	218
GLAFAHQYKNEDACSFTLYGDGASNQGQVFESFNMAKLWNLPV	218
GIAFAMKYRKE KN VCITMFGDGATNQGQLFESMNMAKLWDLPV	238
GIAFADKYRKTGGVVVTTTGDGGSSEGETYEAMNFAKLHEVPC	214
GVALGLKMRGKKAVAITYTGDGGTSQGDFYEGINFAGAFKAPA	188
VAITITGDGGTSQGDFYEGINFAGAFKAPA	196
G.AFA.KYRVTGDGNQGQ.FENMA.LW.LP.	
	250
•	
*3	
IFVVENNUMAIGMSHLRATSDPEIWKKGPAFGMPGVHVDGMDVLKVREVA	299
IFVVENNQWAIGMAHHRSSSIPEIHKKAEAFGLPGIEVDGMDVLAVRQVA	240
ILVCENNHYGMGTAEWRAAKSPSYYKRGD-Y-VPGLKVDGMDAFAVKQAC	266
IFICENNRYGMGTSVERAAASTDYYKRGD-F-IPGLRVDGMDILCVREAT	266
VFCCENNKYGMGTAASRSSAMTEYFKRGQ-Y-IPGLKVNGMDILAVYQAS	286
LYVCENNGYGMGTAAARSSASTDYYTRGD-Y-VPGIWVDGMDVLAVRQAV	262
IFVIENNKWAISTARSEQTKSINFAVKGIATGIPSIIVDGNDYLACIGVF	238
IFVVQNNRFAISTPVEKQTVAKTLAQKAVAAGIPGIQVDGMDPLAVYAAV	246
IFV.ENNGTARK.GPGVDGMD.LAVA.	300
•	
*1 .2	
KEAVTRARRGEGPTLVECETYRFRGHSLADPD-ELRDAAE-KAKYAARDP	247
EKAVERARQGQGPTLIEALTYRFRGHSLADPD-ELRSRQE-KEAWVARDP	347
KFAKQHALE-KGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDP	288
RFAAAYCRSGKGPILMELQTYRYHGHSMSDPGVSYRTREEIQEVRSKSDP	315
KFAKDWCLSGKGPLVLEYETYRYGGHSMSDPGTTYRTRDEIQHMRSKNDP	316
RWAKEWCNAGKGPLMIEMATYRYSGHSMSDPGTSYRTREEVQEVRKTRDP	336
KEVVEYVRKGNGPVLVECDTYRLGAHSSSDNPDAYRPKGEFEEM-AKFDP	312
KAARERAINGEGPTLIETLCFRYGPHTMSGDDPTRYRSKELENEWAKKDP	287
	296
K.AG.GP.L.ETYRY.GHSMSDPYR.R.EDP	
DP	350

APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

FIG. 8C

IAALKKYLIENKLAKEAELKSIEKKIDELVEEAVEFADASPQPGRSQL	2.2-
IKKLKKHILDNQIASSDELNDIQSSVKIDLEQSVEFAMSSPEPNISEL	395
IERIKKLVLSHDLATEKELKDMEKEIRKEVDDAIAKAKDCPMPEPSEL	336
IMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPPLEEL	363
IAGLKMHLIDLGIATEAEVKAYDKSARKYVDEQVELADAAPPPEAKLSIL	364
ITGEKOKIVTAGIVTEDETKEIDKONDKOLDANIOAAPPPEAKLSIL	386
ITGFKDKIVTAGLVTEDEIKEIDKQVRKEIDAAVKQAHTDKESPVELMLT	362
LIRLKQYLIDKKIWSDEQQAQLEAEQDKFVADEFAWVEKNKNYDL-IDIF	336
LVRFRKFLEAKGLWSEEEENNVIEQAKEEIKEAIKKADETPKQKVTDL	344
ILKLA.E.E.KKAP.PL	400
LENVFADPKGFGIGPDGRYRCEDPKFTEG-TAQV	428
KRYLFADN	344
FTNVYVKGFGTESFGPDRKEVKAS-LP	
GYHIYSSDPPFEVRGANQWIKFKSVS	389
FEDVYVKGTETPTLRGRIPEDTWDFKKQGFASRD	390
DIYYNTPAQYVRCTTDEVLQKYLTSEEAVKALAK	420
KYQYDKMDIFLEEQYKEAKEFFEKYPESKEGGHH	396
ISIMFE-ELPFNLKEQYEIYKEKESK	370
THE TOTAL CONTROL OF THE TOTAL	369
••••••	434

FIG. 9A

Plastid A.t. MSSIIHGAGAATTTLSTFNSVDSKKLFVAPSRTNLSVRSQRYIVAGSDAS 50 P.purpurea * A.thaliana H.sapiens S.cerevisiae -A.suum M.capricolum -B.subtilis Consensus KKSFGSGLRVRHSQKLIPNAVATKEADTSASTGHELLLFEALQEGLEEEM ------MSKVFMFDALRAATDEEM 100 MLGILRQRAIDGASTLRRTRFALVSARSYAAGAKEMTVRDALNSAIDEEM 18 ---MAAVSGLVRRPLREVSGLLKRRFHWTAPAALQVTVRDAINQGMDEEL 50 RLPTSLARNVARRAPTSFVRPSAAAAALRFSSTKTMTVREALNSAMAEEL 47 --MAVNGCMRLLRNGLTSACALEQSVRRLASGTLNVTVRDALNAALDEEI 53 ------MAIINNIKAVTDALDCAM 48 18 ----MAQMTMVQAITDALRIEL 18T...AL..A.DEE. 100 Region 1 DRDPHVCVMGEDVGHYGGSYKVTKGLADKFGDLRVLDTPICENAFTGMGI EKDLTVCVIGEDVGHYGGSYKVTKDLHSKYGDLRVLDTPIAENSFTGMAI 150 SADPKVFVMGEEVGQYQGAYKITKGLLEKYGPERVYDTPITEAGFTGIGV 68 ERDEKVFLLGEEVAQYDGAYKVSRGLWKKYGDKRIIDTPISEMGFAGIAV 100 DRDDDVFLIGEEVAQYNGAYKVSKGLLDRFGERRVVDTPITEYGFTGLAV 97 KRDDRVFLIGEEVAQYDGAYKISKGLWKKYGDGRIWDTPITEMAIAGLSV 103 QRDPNVIVFGEDVGTEGGVFRATQGLAVKFGNDRCFNAPISEAMFAGVGL 98 KNDPNVLIFGEDVGVNGGVFRATEGLQAEFGEDRVFDTPLAESGIGGLAI 68 68 .RD..V...GE.VG.Y.G.YK.TKGL..K.G..RV.DTPI.E..F.G... 150 GAAMTGLRPVIEGMNMGFLLLAFNQISNNCGMLHYTSGGQFTIPVVIRGP GAAITGLRPIVEGMNMSFLLLAFNQISNNAGMLRYTSGGNFTLPLVIRGP 200 GAAYAGLKPVVEFMTFNFSMQAIDHIINSAAKSNYMSAGQINVPIVFRGP 118 GAAMAGLRPICEFMTFNFSMQAIDQVINSAAKTYYMSGGLQPVPIVFRGP 150 GAALKGLKPIVEFMSFNFSMQAIDHVVNSAAKTHYMSGGTQKCQMVFRGP 147 153





CA AMMICI PRICE-	
GAAMNGLRPICEFMSMNFSMQGIDHIINSAAKAHYMSAGRFHVPIVFRGA	140
	148 118
GLALQGFRPVPEIQFFGFVYEVMDSICGQMARIRYRTGGRYHMPITIRSP	
	118
GAAGLRPE.MFA.D.I.N.AAY.SGGP.V.RGP	200
· · · · · · · · · · · · · · · · · · ·	200
•	
CGVCPOLCA ENGODY Town Region 2	
GOVGRQLIGAEHSURLESYFOST PGTOMVA CCERRIANT TO THE POPULATION OF THE	250
TO SECOND STATE OF THE SECOND STATE AND THE SECOND	168
	200
THE PROPERTY OF THE PROPERTY O	
	197
	203
	198
FGGGVHTPELHSDSLEGLVAQQPGLKVVIPSTPYDAKGLILAAIDSPDPV	168
	168
.GA.HSQAPGLKVV.PDAKGLLKAAIRD.NPV	
THE DECEMBER OF THE PROPERTY O	250
TT DELICATION OF THE PROPERTY	
ILFEHVLLYNLKEKIPDEDYICNLEEAEMVRPGEHITILTYSRMRY	
	296
	214
	250
	247
	252
	248
IFLEHLKLYRSFRQEVPEGEYTIPIGKADIKREGKDITIIAYGAMVH	215
	215
LELLYEP.GKA.I.R.G.DITIVTYSV.	
January State of the State of t	300
Region 3	
HVMQAAKTLVNKGYDPEVIDIRSI.KPEDIUTIGNG	
GIDERADI SUKDI DIDCI GIGITICI	344
	262
	298
	295
The state of the contract of t	301
	296
ESLKAAAELEKEGISAEVVDLRTVQPLDIETIIGSVEKTGRAIVVQEA	265
	263
L.AALGEVI.LRSPLDTISV.KT.RLVEE.	
	350
Region 4	
MRTGGIGASLTAAINE-NFHDYLDAPVMCLSSQDVPTPYAGTLEEWTVVQ	
TARE TO THE EMILY VO	393

FIG. 9C

MKTAGIGAELIAOINE-HLEDELDA DIZIDLIGGODITATION	
MKTAGIGAELIAQINE-HLFDELDAPVVRLSSQDIPTPYNGSLEQATVIQ	311
FPQHGVCAEICASVVE-ESFSYLDAPVERIAGADVPIPYTANLERLALPQ	347
WPQFGVGAEICARIMEGPAFNFLDAPAVRVTGADVPMPYAKILEDNSIPQ	345
TISTGVGAETVAQVMESEAFDYLDAPTORVTGADVDTDVA KDI HD HT	351
WINCG VGAETSARVIESDAFGYLDGPTI.RVTGVDVDMDVAODI ETTA A	346
VIOLO VOMETTAT VINE - ECFEYTKAPI SECTEVDAT TREDEG TOWNS	313
QRQAGIAANVVAEINE-RAILSLEAPVLRVAAPDTVYPFAQA-ESVWLPN	
	311
GVGAEI.AEF.YLDAPRG.DVP.PYALEPQ	400
•	400
PAQIVTAVEQLCQ	
PHQIIDAVKNIVNSSKTITT	406
IEDIVRASKRACYRSK	331
VKDIIFAIKKTLNI	363
TPTIVKAVKEVLSIE	359
PADVVKMVKKCLNVQ	366
PKKVLVKMQELLDFKF	361
FKDVIETAKKVMNF	329
I I I I I I I I I I I I I I I I I I I	325
7	223
IA.K	420

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FIG: 10A

A. t.	MAALLG-RSCRKLSFPSLTHG	355
Human	THE VARAGOULD RECARDED A TEXT OF THE ACTION A TEXT OF THE ACTION AS TO THE ACTION AS	30000
Bovine	MAAVAAFAGWLLRLRAAGADGPWRRLCGAGLSRGFLQSASAY-GA	AQRRQ 50
	- A - CT MEGAGDS KG F DQSASAY - GA	AQRRQ 49
Consensus	MAAVAA.AGWLLRLRAAGA.G.WRRL.GAGL.RGFLAA	
	A CONTROL OF THE PROPERTY OF T	AQRRQ 50
V	STETGKPLNLYSAINQALHIALDTDPRSYVFGEDVGF	
VAHETEOPD	PEDREYCOTOKMNI FOGUMGA TOTAL	61
VAHETEODO	PEPREYGQTQKMNLFQSVTSALDNSLAKDPTAVIFGEDVAF	100
VAII IF QFD	PEPVEYGQTQKMNLFQAVTSALDNSLAKDPTAVIFGEDVAF	99
VAHFTFQPDI	PEP.EYGQTQKMNLFQAVTSALDNSLAKDPTAVIFGEDVAF	100
•		100
	•	
GGVFRCTTGL	AERFGKNRVFNTPLCEQGIVGFGIGLAAMGNRAIVEIQFA	4
GGVFRCTVGL	RDKYGKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFA	111
GGVFRCTVGL	RDKYGKDRVFNTPLCEQGIVGFGIGIAVIGATAIAEIQFA	150
GGVFRCTVGI	PDKYCKDBYENEDI CEOGTYGEGIGIAVIGATAIAEIQFA	149
	RDKYGKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFA	150
·		
DYIYPAFDQI	VNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSP	161
DITLEMEDOT	VNEAAKYRYRSGDLFNCGSLTTRSPWCCVCUCALVUGOGR	
DYIFPAFDQI	VNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	200
	THE THE TWO CVONGALINSUSP	199
DYIFPAFDOI	NEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	
~	THE PWGCVGHGALYHSQSP	200
	•	
EAFECUUDCE	TIVI DDGDDD WG	
PAPPAHODOTE	CVVIPRSPREAKGLLLSCIRDPNPVVFFEPKWLYRQAVEE	211
EAFFARCPGIK	VVIPRSPFQAKGLLLSCIEDKNDCIEEEDVIIVDAAADD	250
EAFFAHCPGIK	VVVPRSPFQAKGLLLSCIEDKNPCIFFEPKILYRAAVEQ	249
		273
EAFFAHCPGIK	VVIPRSPFQAKGLLLSCIEDKNPCIFFEPKILYRAAVEE	250
		250

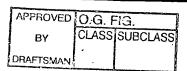






FIG. 10B

VPEHDYMIPLSEAEVIREGNDITLVGWGAQLTVMEQ-ACLDAEKEGISCE VPIEPYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVASMAKEKLGVSCE VPVEPYNIPLSQAEVIQEGSDVTLVAWGTQVHEIREVAAMAQEKLGVSCE	260 300 299
VP.EPYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVA.MA.EKLGVSCE	300
I IDI WILL DUDWING	
LIDLKTLLPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISATILERCF	310
VIDERTIIPWDVDTICKSVIKSGRLLISHEAPLTGGEASEISSTVORDGR	350
VIDLRTILPWDVDTVCKSVIKTGRLLVSHEAPLTGGFASEISSTVQEQCF	349
VIDLRTILPWDVDTVCKSVIKTGRLLISHEAPLTGGFASEISSTVQE.CF	350
I WI EN DUGDING	
LKLEAPVSRVCGLDTPFPLVFEPFYMPTKNKILDAIKSTVNY	352
LNLEAPISRVCGYDTPFPHIFEPFYIPDKWKCYDALRKMINY	392
LNLEAPISRVCGYDTPFPHIFEPFYIPDKWKCYDALRKMINY	391
LNLEAPISRVCGYDTPFPHIFEPFYIPDKWKCYDALRKMINY	392